L Number	Hits	Search Text	DB	Time stamp
1	7996	microarray and design$ and analys$	USPAT; US-PGPUB; EPO; JPO; DERWENT; IBM_TDB	2004/08/06 17:32
2	435	(microarray near10 design$) and analys$	USPAT; US-PGPUB; EPO; JPO; DERWENT; IBM_TDB	2004/08/06 17:32
4	424	(microarray near10 design$) and analys$	USPAT; US-PGPUB	2004/08/06 17:33
5	22693	435/6[ccls]	USPAT; US-PGPUB	2004/08/06 17:33
6	1482	702/19[ccls]	USPAT; US-PGPUB	2004/08/06 17:33
7	984	702/20[ccls]	USPAT; US-PGPUB	2004/08/06 17:33
8	121	435/6[ccls] and 702/19[ccls] and 702/20[ccls]	USPAT; US-PGPUB	2004/08/06 17:33
9	24025	435/6[ccls] or 702/19[ccls] or 702/20[ccls]	USPAT; US-PGPUB	2004/08/06 17:33
3	11	(microarray near10 design$) and analys$	EPO; JPO; DERWENT; IBM_TDB	2004/08/06 17:34
10	282	((microarray near10 design$) and analys$) and (435/6[ccls] or 702/19[ccls] or 702/20[ccls])	USPAT; US-PGPUB	2004/08/06 17:34

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James Martinell
Primary Examiner 1631

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          SDIs in CAplus
 NEWS 6 May 27  CAplus super roles and document types
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CASREACT
 NEWS 8 Jun 28  ANTE, AQUALINE, BIOENG, CIVILENG,
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=> s (microarray? (10a) design?)/bi,ab
      23238 MICROARRAY?/BI
      11452 MICROARRAY?/AB
     686660 DESIGN?/BI
     622610 DESIGN?/AB
L1       517 (MICROARRAY? (10A) DESIGN?)/BI,AB

=> s l1 and analys?/bi,ab
    1771034 ANALYS?/BI
     423125 ANALYS?/AB
L2       179 L1 AND ANALYS?/BI,AB

=> s l2 not 2004/py
     643457 2004/PY
L3       148 L2 NOT 2004/PY

=> s l3 not 2003/py
    1161611 2003/PY
L4        87 L3 NOT 2003/PY

=> s l4 not 2002/py
    1130080 2002/PY
L5        39 L4 NOT 2002/PY

=> s l5 not 2001/py
    1077284 2001/PY
L6        15 L5 NOT 2001/PY
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FILE 'CAPLUS' ENTERED AT 18:04:29 ON 06 AUG 2004
L1 517 S (MICROARRAY? (10A) DESIGN?)/BI,AB
L2 179 S L1 AND ANALYS?/BI,AB
L3 148 S L2 NOT 2004/PY
L4 87 S L3 NOT 2003/PY
L5 39 S L4 NOT 2002/PY
L6 15 S L5 NOT 2001/PY

=> d l6 1-15 bib ab

L6 ANSWER 1 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:341190 CAPLUS Full-text
DN 136:80467
TI Cluster inference methods and graphical models evaluated on NCI60
microarray gene expression data
AU Waddell, Peter J.; Kishino, Hirohisa
CS Chugai Research Institute for Molecular Medicine, Ibaraki, 300-4101, Japan
SO Genome Informatics Series (2000), 11(Genome Informatics 2000), 129-140
CODEN: GINSE9; ISSN: 0919-9454
PB Universal Academy Press
DT Journal
LA English
AB At present, there is a lack of a sound methodol. to infer causal gene expression relationships on a genome wide basis. We address this first by examining the behavior of some of the latest and fastest algorithms for tree and cluster anal., particularly hierarchical methods popular in phylogenetics. Combined with these are two novel distances based on partial, rather than full, correlations. Theor., partial correlations should provide better evidence for regulatory genetic links than standard correlations. To compare the clusters obtained by many alternative methods we use tree consensus methods. To compare methods of anal. we used tree partition metrics followed by another level of clustering. These, and a tree fit metric, all suggest that the new distances give quite different trees than those usually obtained. In the second part we consider graphical modeling of the interactions of important genes of the cell cycle. Despite the models seeming to fit well on occasions, and despite the exptl. error structure seeming close to multivariate normal, there are considerable problems to overcome. Latent variables, in this case important genes missing from the anal., are inferred to have a strong effect on the partial correlations. Also, the data show clear evidence of sampling distributions conditional on the status of important cancer related genes, including TP53. Without full information on which genes are wild type the appropriate models cannot be fitted. These findings point to the need to include and distinguish not only all relevant genes but also all splice variants in the **design** phase of a **microarray** anal. Failure to do so will induce problems similar to both latent variables and conditional distributions.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:64500 CAPLUS Full-text
DN 135:147899
TI Assessing reliability of gene clusters from gene expression data
AU Zhang, Kui; Zhao, Hongyu
CS Department of Epidemiology and Public Health, Yale University School of
Medicine, New Haven, CT, 06520, USA
SO Functional & Integrative Genomics (2000), 1(3), 156-173
CODEN: FIGUBY; ISSN: 1438-793X
PB Springer-Verlag
DT Journal
LA English
AB The rapid development of **microarray** technologies has raised many challenging problems in experiment **design** and data anal. Although many numerical algorithms have been successfully applied to analyze gene expression data, the effects of variations and uncertainties in measured gene expression levels across samples and expts. have been largely ignored in the literature. In this article, in the context of hierarchical clustering algorithms, the authors introduce a statistical resampling method to assess the reliability of gene clusters identified from any hierarchical clustering method. Using the clustering trees constructed from the resampled data, the authors can evaluate the confidence value for each node in the observed clustering tree. A majority-rule consensus tree can be obtained, showing clusters that only occur in a majority of the resampled trees. The authors illustrate the proposed methods with applications to two published data sets. Although the methods are discussed in the context of hierarchical clustering methods, they can be applied with other cluster-identification methods for gene expression data to assess the reliability of any gene cluster of interest.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 3 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:841063 CAPLUS Full-text
TI Detecting gene copy number fluctuations in tumor cells by microarray
analysis of genomic representations
AU Lucito, Robert; West, Joseph; Reiner, Andrew; Alexander, Joan; Esposito,
Diane; Mishra, Bhubaneswar; Powers, Scott; Norton, Larry; Wigler, Michael
CS Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 11724, USA
SO Genome Research (2000), 10(11), 1726-1736
CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal; Letter
LA English
AB In this work, we explore the use of representations in conjunction with DNA microarray technol. to measure gene copy number changes in cancer. We demonstrate that arrays of DNA probes derived from low-complexity representations can be used to detect amplifications, deletions, and polymorphic differences when hybridized to representations of genomic DNA. The method is both reproducible and verifiable, and is applicable even to microscopic amts. of primary tumors. We also present a math. model for array performance that is useful for **designing** and understanding DNA **microarray** hybridization protocols. The future applications and challenges of this approach are discussed.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 4 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:783946 CAPLUS Full-text
DN 135:117868
TI General nonlinear framework for the **analysis** of gene interaction
via multivariate expression arrays
AU Kim, Seungchan; Dougherty, Edward R.; Bittner, Michael L.; Chen, Yidong;
Sivakumar, Krishnamoorthy; Meltzer, Paul; Trent, Jeffrey M.
CS Department of Electrical Engineering, Texas A&M University, College
Station, TX, 77843-3128, USA
SO Journal of Biomedical Optics (2000), 5(4), 411-424
CODEN: JBOPFO; ISSN: 1083-3668
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB A cDNA microarray is a complex biochem.-optical system whose purpose is the simultaneous measurement of gene expression for thousands of genes. In this paper the authors propose a general statistical approach to finding assocns. between the expression patterns of genes via the coefficient of determination This coefficient measures the degree to which the transcriptional levels of an observed gene set can be used to improve the prediction of the transcriptional state of a target gene relative to the best possible prediction in the absence of observations. The method allows incorporation of knowledge of other conditions relevant to the prediction, such as the application of particular stimuli or the presence of inactivating gene mutations, as predictive elements affecting the expression level of a given gene. Various aspects of the method are discussed: prediction quantification, unconstrained prediction, constrained prediction using ternary perceptrons, and **design** of predictors given small nos. of replicated **microarrays.** The method is applied to a set of genes under-going genotoxic stress for validation according to the manner in which it points toward previously known and unknown relationships. The entire procedure is supported by software that can be applied to large gene sets, has a number of facilities to simplify data anal., and provides graphics for visualizing exptl. data, multiple gene interaction, and prediction logic.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 5 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:633188 CAPLUS Full-text
DN 134:111198
TI Importance of replication in microarray gene expression studies: statistical methods and evidence from repetitive cDNA hybridizations
AU Lee, Mei-Ling Ting; Kuo, Frank C.; Whitmore, G. A.; Sklar, Jeffrey
CS Department of Medicine, Brigham and Women's Hospital, Boston, MA, 02115,
USA
SO Proceedings of the National Academy of Sciences of the United States of
America (2000), 97(18), 9834-9839
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB We present statistical methods for analyzing replicated cDNA microarray expression data and report the results of a controlled experiment The study was conducted to investigate inherent variability in gene expression data and the extent to which replication in an experiment produces more consistent and reliable findings. We introduce a statistical model to describe the probability that mRNA is contained in the target sample tissue, converted to probe, and ultimately detected on the slide. We also introduce a method to analyze the combined data from all replicates. Of the 288 genes considered in this controlled experiment, 32 would be expected to produce strong hybridization signals because of the known presence of repetitive sequences within them. Results based on individual replicates, however, show that there are 55, 36, and 58 highly expressed genes in replicates 1, 2, and 3, resp. On the other hand, an anal. by using the combined data from all 3 replicates reveals that only 2 of the 288 genes are incorrectly classified as expressed. Our experiment shows that any single microarray output is subject to substantial variability. By pooling data from replicates, we can provide a more reliable anal. of gene expression data. Therefore, we conclude that designing expts. with replications will greatly reduce misclassification rates. We recommend that at least three replicates be used in **designing** expts. by using cDNA **microarrays,** particularly when gene expression data from single specimens are being analyzed.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 6 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:401188 CAPLUS Full-text
DN 134:158143
TI The Lymphochip: a specialized cDNA microarray for the genomic-scale
analysis of gene expression in normal and malignant lymphocytes
AU Alizadeh, A.; Eisen, M.; Davis, R. E.; Ma, C.; Sabet, H.; Tran, T.; Powell, J. I.; Yang, L.; Marti, G. E.; Moore, D. T.; Hudson, J. R., Jr.;
Chan, W. C.; Greiner, T.; Weisenburger, D.; Armitage, J. O.; Lossos, I.;
Levy, R.; Botstein, D.; Brown, P. O.; Staudt, L. M.
CS Metabolism Branch, National Institutes of Health, Bethesda, MD, 20892, USA
SO Cold Spring Harbor Symposia on Quantitative Biology (1999), 64(Signaling
and Gene Expression in the Immune System), 71-78
CODEN: CSHSAZ; ISSN: 0091-7451
PB Cold Spring Harbor Laboratory Press
DT Journal; General Review
LA English
AB A review and discussion with 32 refs. of the **design** and application of a cDNA **microarray** enriched for genes that are preferentially expressed in lymphoid cells or are of known immunol. or oncol. importance. Gene expression in B-lymphocyte development and in B-cell lymphomas has been studied using the Lymphochip.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 7 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:354378 CAPLUS Full-text
DN 134:110979
TI Spot checks: automation in microarray image processing and gene expression
on **analysis** speeds up drug discovery
AU Kuklin, Alexander

CS BioDiversity, Inc., Mountain View, CA, USA
SO Modern Drug Discovery (2000), 3(4), 52-54
CODEN: MDDIFT; ISSN: 1099-8209
PB American Chemical Society
DT Journal; General Review
LA English
AB A review with 3 refs. on automation and integration of microarray data management.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 8 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:333916 CAPLUS Full-text
DN 134:142403
TI Automated **analysis** of multivariate nonlinear gene relations based on cDNA microarray expression data
AU Kim, Seungchan; Dougherty, Edward R.; Bittner, Michael L.; Chen, Yidong;
Sivakumar, Krishnamoorthy; Meltzer, Paul S.; Trent, Jeffrey M.
CS Dep. Electr. Eng., Texas A&M Univ., USA
SO Proceedings of SPIE-The International Society for Optical Engineering
(2000), 3926(Advances in Nucleic Acid and Protein Analyses, Manipulation,
and Sequencing), 150-155
CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB A cDNA microarray is a complex biochem.-optical system whose purpose is the simultaneous measurement of gene expression for thousands of genes. This paper describes a general statistical environment for finding assocns. among gene expression patterns, and between genes and external conditions, via the coefficient of determination This coefficient measures the degree to which the transcriptional levels of an observed gene set can be used to improve the prediction of the transcriptional state of a target gene relative to the best possible prediction in the absence of observations. Various aspects of the method are discussed: prediction quantification, **design** of predictors given small nos. of replicated **microarrays**, and constrained prediction using ternary perceptrons. A main focus is the supporting software and its facilities for data anal. and visualization.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 9 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:263599 CAPLUS Full-text
DN 133:160266
TI Overview of a **microarray** scanner: **design** essentials for an integrated acquisition and **analysis** platform
AU Basarsky, Trent; Verdnik, Damian; Zhai, Jack Ye; Wellis, David
CS Axon Instruments, Inc., Foster City, CA, USA
SO Microarray Biochip Technology (2000), 265-284. Editor(s): Schena, Mark.
Publisher: Eaton Publishing Co., Natick, Mass.
CODEN: 68VMAZ
DT Conference; General Review
LA English
AB A review with 15 refs. Data quality form hardware and data anal. and confidence measure from software form the basis of a well **designed microarray** scanner and data extraction software system. Successful hardware design is only possible if one has a deep understanding and experience of optical and electronic technologies, whereas the usability and efficiency of such a system is derived form the tightly integrated communication between hardware and software, including optimized algorithms and and a thoughtful and easy to use software interface. The final requirement of cost can be met by offering the scanner and multiple copies of the acquisition and anal. software at a value price point attractive to both academia an industry, as accomplished with the GenePix 4000. The future of microarray scanning and anal. can be summarized in one word: automation. On the software side, there is not yet an anal. package that can extract the data from a microarray without human intervention, but existing software is rapidly approaching this point. Anal. of dataset from multiple arrays is already offered, but not as a component of a completely integrated system. On both the hardware and software sides, full automation is not far off for integrated scanning and anal. systems.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 10 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:263592 CAPLUS Full-text
DN 134:66728
TI Large-scale genomic **analysis** using Affymetrix GeneChip probe arrays
AU Warrington, Janet A.; Dee, Suzanne; Trulson, Mark
CS Affymetrix, Inc., Santa Clara, CA, USA
SO Microarray Biochip Technology (2000), 119-148. Editor(s): Schena, Mark.
Publisher: Eaton Publishing Co., Natick, Mass.
CODEN: 68VMAZ
DT Conference; General Review
LA English
AB A review with 50 refs. of the GeneChip® system from Affymetrix. Topics include: a brief overview of the characteristics of the technol. that distinguish it from other DNA **microarray** hybridization technologies; an introduction to array **design**, probe selection, and array synthesis; a description of current applications including results from recent expts.; and a brief discussion on future applications.
RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 11 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:782490 CAPLUS Full-text
DN 132:132868
TI Rapid **analysis** of gene expression (RAGE) facilitates universal expression profiling
AU Wang, Aijin; Pierce, Angela; Judson-Kremer, Kimberly; Gaddis, Sara; Aldaz,
C. Marcelo; Johnson, David G.; MacLeod, Michael C.
CS Department of Carcinogenesis, University of Texas M. D. Anderson Cancer
Center, Smithville, TX, 78957, USA
SO Nucleic Acids Research (1999), 27(23), 4609-4618
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB Current techniques for anal. of gene expression either monitor one gene at a time, for example northern hybridization or RT-PCR methods, or are **designed** for the simultaneous anal. of thousands of genes, for example **microarray** hybridization or serial anal. of gene

expression. To provide a flexible, intermediate scale alternative, a PCR-based method for the rapid anal. of gene expression has been developed which allows expression changes to be determined in either a directed search of known genes, or an undirected survey of unknown genes. A single set of reagents and reaction conditions allows **analyses** of most genes in any eukaryote. The method is useful for assaying on the order of tens to hundreds of genes in multiple samples. Control expts. indicate reliable detection of changes in gene expression 2-fold and greater, and sensitivity of detection better than 1 in 10 000. **Analyses** of over 400 genes in a mouse system transgenic for the E2F1 gene have identified several new downstream targets of E2F1, including Brca1 and Cdk7, in addition to several unidentified genes that are upregulated in the transgenic mice. Changes in expression of several genes related to apoptosis suggest a possible potentiation of apoptotic pathways in the transgenic keratinocytes.

RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 12 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:496131 CAPLUS Full-text
DN 131:282038
TI High density oligonucleotide and DNA probe arrays for the **analysis** of target DNA
AU Thompson, Michael; Michelle Furtado, L.
CS Department of Chemistry, University of Toronto, Toronto, ON, M5S 3H6, Can.
SO Analyst (Cambridge, United Kingdom) (1999), 124(8), 1133-1136
CODEN: ANALAO; ISSN: 0003-2654
PB Royal Society of Chemistry
DT Journal; General Review
LA English
AB A review, with 19 refs. The acquisition of sequence, expression and other information concerning genetic material constitutes a crucial component of the modern revolution in mol. biol. One important advance in this area is the development of high d. oligonucleotide/DNA microarrays which allows the rapid sequence anal. of genomic target samples in addition to diagnostic possibilities with respect to genetic and infectious disease. In the present article we review protocols for the **design** of such **microarrays** and their principles of operation. Together with a look at some recent applications we include brief remarks as to the possibilities for the future.

RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:46716 CAPLUS Full-text
TI High-throughput quantitative histological **analysis** of alzheimer's disease pathology using a confocal digital microscanner
AU Hanzel, David K.; Trojanowski, John Q.; Johnston, Richard F.; Loring, Jeanne F.
CS Molecular Dynamics, Inc., Sunnyvale, CA, 94086, USA
SO Nature Biotechnology (1999), 17(1), 53-57
CODEN: NABIF9; ISSN: 1087-0156
PB Nature America
DT Journal
LA English
AB To develop a rapid method of quantifying immunohistochem. information in tissue sections, we tested a confocal laser fluorescence microscanner initially **designed** for DNA **microarray** anal. This instrument collects digital images at multiple wavelengths, scans entire sections at a resolution of 5 or 10 μm in less than 10 min, and quantifies structures labeled with fluorescent or nonfluorescent probes. We assessed the microscanner by studying immunostained amyloid plaques in the Alzheimer's disease (AD) brain and in the brain of a transgenic mouse model of AD amyloidosis, as efforts to correlate measures of amyloid plaques in brain sections with behavioral impairments are impeded by limitations in current morphometric methods. Microscanner anal. was used to determine amyloid burden in the occipital morphometric methods. Microscanner anal. was used to determine amyloid burden in the occipital and entorhinal cortices of the mouse (3.7%) and human AD brain (1.6%). We also quantified the colocalization of plaque β-amyloid (Aβ) with glial fibrillary acidic protein, a marker of gliosis (mouse 0.9%, human AD 3.7%). The microscanner may be generally applicable to a wide variety of human histopathologies and their animal models, wherever rapid unbiased quant. anal. is needed.

L6 ANSWER 14 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:24743 CAPLUS Full-text
DN 130:204614
TI The integration of microarray information in the drug development process
AU Braxton, Scott; Bedilion, Tod
CS Synteni Inc., Fremont, CA, 94555, USA
SO Current Opinion in Biotechnology (1998), 9(6), 643-649
CODEN: CUOBE3; ISSN: 0958-1669
PB Current Biology Publications
DT Journal; General Review
LA English
AB A review with 37 refs. In the past year, microarray technologies have moved beyond the proof-of-principle stage. Microarrays are now being used for genome-wide expression monitoring, large-scale polymorphism screening and mapping, and for the evaluation of drug candidates.

RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 15 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:110468 CAPLUS Full-text
DN 124:137802
TI Method and apparatus for fabricating microarrays of biological samples
IN Shalon, Tidhar Dari; Brown, Patrick O.
PA Board of Trustees of the Leland Stanford Junior University, USA
SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9535505	A1	19951228	WO 1995-US7659	19950616
W: AU, CA, JP				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 5807522	A	19980915	US 1995-477809	

19950607
AU 9528629 A1 19960115 AU 1995-28629
19950616
AU 709276 B2 19990826
EP 804731 A1 19971105 EP 1995-923921
19950616
EP 804731 B1 19990526
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE
JP 10503841 T2 19980407 JP 1995-502498
19950616
PRAI US 1994-261388 A 19940617
US 1995-477809 A 19950607
WO 1995-US7659 W 19950616

AB A method and app. for forming microarrays of biol. samples on a support are disclosed for, e.g., large-scale screening assays, such as arrays of DNA samples to be used in DNA hybridization assays for genetic research and diagnostic applications. The method involves dispensing a known volume of a reagent at each of a selected array position, by tapping a capillary dispenser on the support under conditions effective to draw a defined volume of liquid onto the support. The apparatus is **designed** to produce a **microarray** of such regions in an automated fashion.

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